

TABLE S1. Concentration of different polymer species in versions of the model

Model version:	Isodesmic Assembly	$\epsilon = 1 \times 10^{-4}$	Monomer Activation + Isodesmic Assembly	Segregated Assembly of L_n and H_n	Only One End Changes Conformation
Cooperative?	No	Yes	Yes	Yes	No
Equilibrium constants					
K_C	0	1×10^{-4}	1×10^{-4}	1×10^{-4}	1×10^{-4}
K_{LL} (μM)	1	1×10^{-4}	0	1×10^{-4}	1×10^{-4}
K_{LH} (μM)	0	1×10^{-4}	0	0	1×10^{-4}
K_{HH} (μM)	0	1×10^{-4}	1×10^{-4}	1×10^{-4}	1×10^{-4}
K_{HL} (μM)	0	1×10^{-4}	0	0	1×10^{-4}
Concentrations of polymer species at equilibrium* (μM)					
L	7.30×10^{-1}	9.97×10^{-1}	9.97×10^{-1}	9.97×10^{-1}	7.30×10^{-1}
H	0	9.97×10^{-5}	9.97×10^{-5}	9.97×10^{-5}	7.30×10^{-5}
<i>monomer</i>	<i>7.30×10^{-1}</i>	<i>9.97×10^{-1}</i>	<i>9.97×10^{-1}</i>	<i>9.97×10^{-1}</i>	<i>7.30×10^{-1}</i>
LL	5.33×10^{-1}	9.93×10^{-5}	0	9.93×10^{-5}	5.33×10^{-5}
HL	0	9.93×10^{-9}	0	0	5.33×10^{-1}
LH	0	9.93×10^{-9}	0	0	5.33×10^{-9}
HH	0	9.93×10^{-5}	9.93×10^{-5}	9.93×10^{-5}	5.33×10^{-5}
<i>dimer</i>	<i>5.33×10^{-1}</i>	<i>1.99×10^{-4}</i>	<i>9.93×10^{-5}</i>	<i>1.99×10^{-4}</i>	<i>5.33×10^{-1}</i>
LLL	3.89×10^{-1}	9.90×10^{-9}	0	9.90×10^{-9}	3.89×10^{-9}
HLL	0	9.90×10^{-13}	0	0	3.89×10^{-5}
LHL	0	9.90×10^{-13}	0	0	3.89×10^{-5}
LLH	0	9.90×10^{-13}	0	0	3.89×10^{-13}
HHL	0	9.90×10^{-9}	0	0	3.89×10^{-1}
HLH	0	9.90×10^{-17}	0	0	3.89×10^{-9}
LHH	0	9.90×10^{-9}	0	0	3.89×10^{-9}
HHH	0	9.90×10^{-5}	9.90×10^{-5}	9.90×10^{-5}	3.89×10^{-5}
<i>trimer</i>	<i>3.89×10^{-1}</i>	<i>9.90×10^{-3}</i>	<i>9.90×10^{-3}</i>	<i>9.90×10^{-3}</i>	<i>3.89×10^{-1}</i>
LLLL	2.84×10^{-1}	9.87×10^{-13}	0	9.87×10^{-13}	2.84×10^{-13}
HLLL	0	9.87×10^{-17}	0	0	2.84×10^{-9}
LHLL	0	9.87×10^{-17}	0	0	2.84×10^{-9}
LLHL	0	9.87×10^{-17}	0	0	2.84×10^{-9}
LLLH	0	9.87×10^{-17}	0	0	2.84×10^{-17}
HHLL	0	9.87×10^{-13}	0	0	2.84×10^{-5}
HLHL	0	9.87×10^{-21}	0	0	2.84×10^{-5}
HLLH	0	9.87×10^{-21}	0	0	2.84×10^{-13}
LHHL	0	9.87×10^{-13}	0	0	2.84×10^{-5}
LHLH	0	9.87×10^{-21}	0	0	2.84×10^{-13}
LLHH	0	9.87×10^{-13}	0	0	2.84×10^{-13}
LHHH	0	9.87×10^{-9}	0	0	2.84×10^{-9}
HLHH	0	9.87×10^{-17}	0	0	2.84×10^{-9}
HHLH	0	9.87×10^{-17}	0	0	2.84×10^{-9}
HHHL	0	9.87×10^{-9}	0	0	2.84×10^{-1}
HHHH	0	9.87×10^{-5}	9.87×10^{-5}	9.87×10^{-5}	2.84×10^{-5}
<i>tetramers</i>	<i>2.84×10^{-1}</i>	<i>9.87×10^{-3}</i>	<i>9.87×10^{-3}</i>	<i>9.87×10^{-3}</i>	<i>2.8×10^{-1}</i>

*Results were calculated for 10 μM total protein (z_0). In bold are the most abundant species of each length. In italics are the total concentration of polymers of each length.

Figure S1. *Determining which combination of parameters produce the greatest cooperativity.* In cooperative systems, polymer does not assemble unless the equilibrium monomer concentration has nearly reached its maximum possible value. Therefore, in a plot of p versus z_I , ideally cooperative systems will exhibit a sharp 90° bend upwards; the closer a curve is to this ideal, the more cooperative the system. (A) In cooperative systems, K_{HH} must be large and all other parameters small. The five equilibrium constants were set equal to 1, 0.1, or 10 in all combinations. For each combination of values, p and z_I were first calculated for a range of L concentrations, then normalized by dividing by z_I^∞ . Arrow: The greatest cooperativity is seen in the right-most trajectory, where $K_{HH} = 10$ while all other equilibrium constants = 0.1. Arrowhead: Isodesmic polymerization with all K 's = 1 is in the middle of the data sets. (B) Nearly ideal cooperativity can be produced when equilibrium constants are varied over a wider range. Here, K_C, K_{LL}, K_{LH} , and $K_{HL} = \epsilon$ and $K_{HH} = 1/\epsilon$ for $\epsilon = 1, 1 \times 10^{-2}, 1 \times 10^{-4}$, and 1×10^{-6} . The left hand, least sharply curved line is for $\epsilon = 1$, isodesmic polymerization. As ϵ decreases, polymerization approaches ideal cooperativity.

